## SEQUENCE LISTING

<110> BEASLEY, Ellen et al <120> ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF <130> CL001078DIV <160> 5 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 1864 <212> DNA <213> Homo sapiens <400> 1 cgagtgcgct gctgagtcct gtagataaag ccgccaaccc cggggactgg tgtctcctga 60 gtgaccgtgc agccgtgggc gccatagaaa gcagagaagg cagtgaactt cgaccacttc 120 cagateette gggecattgg gaagggeage tttggeaagg tgtgcattgt geagaagegg 180 gacacggaga agatgtacgc catgaagtac atgaacaagc agcagtgcat cgagcgcgac 240 gaggteegea acgtetteeg ggagetggag atcetgeagg agategagea egtetteetg 300 gtgaacctct ggtactcctt ccaggacgag gaggacatgt tcatggtcgt ggacctgcta 360 ctgggcgggg acctgcgcta ccacctgcag cagaacgtgc agttctccga ggacacggtg 420 aggetgtaca tetgegagat ggeactgget etggaetace tgegeggeea geacateate 480 cacagagatg tcaagcctga caacattctc ctggatgaga gaggacatgc acacctgacc 540 gacttcaaca ttgccaccat catcaaggac ggggagcggg cgacggcatt agcaggcacc 600 aagccgtaca tggctccgga gatcttccac tcttttgtca acggcgggac cggctactcc 660 ttcgaggtgg actggtggtc ggtgggggtg atggcctatg agctgctgcg aggatggagg 720 ccctatgaca tccactccag caacgccgtg gagtccctgg tgcagctgtt cagcaccgtg 780 agegtecagt atgtececae gtggtecaag gagatggtgg cettgetgeg gaageteete 840 actgtgaacc ccgagcaccg gctctccagc ctccaggacg tgcaggcagc cccggcgctg 900 geeggegtge tgtgggaeca eetgagegag aagagggtgg ageegggett egtgeecaac 960 aaaggccgtc tgcactgcga ccccaccttt gagctggagg agatgatcct ggagtccagg 1020 cccctgcaca agaagaagaa gcgcctggcc aagaacaagt cccgggacaa cagcagggac 1080 ageteceagt eegagaatga etatetteaa gaetgeeteg atgeeateea geaagaette 1140 gtgattttta acagagaaaa gctgaagagg agccaggacc tcccgaggga gcctctcccc 1200 gcccctgagt ccagggatgc tgcggagcct gtggaggacg aggcggaacg ctccgccctg 1260 cccatgtgcg gccccatttg cccctcggcc gggagcgct aggccgggac gcccgtggtc 1320 ctcaccctt gagctgcttt ggagactcgg ctgccaqagg gagggccatg ggccgaggcc 1380 tggcattcac gttcccaccc agcctggctg gcggtgccca cagtgccccg gacacatttc 1440 acacctcagg ctcgtggtgg tgcaggggac aagaggctgt gggtgcaggg gacacctgtg 1500 gagggcattt cccgtgggcc cccgagaccc gcctagatgg aggaagcgct gctgggcgcc 1560. ctcttaccgc tcacggggag ctggggccat ggatgggaca ggagtctttg tccctgctca 1620 gcccggaggc tgtgcacggc cctcgtcaca aggtgaccct tgcagcacag gccgcgggtg 1680 ccccaggete ggeteagtte ttggaggtea agggeatggg ttggggtagt gggtggggag 1740 gtgaatgttt totagagatt caaactgctc cagcaatttc tgtatagttt tcacctctga 1800 aaaa 1864 <210> 2 <211> 369

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Val Asn Phe Asp His Phe Gln Ile Leu Arg Ala Ile Gly Lys Gly Ser 5 10 Phe Gly Lys Val Cys Ile Val Gln Lys Arg Asp Thr Glu Lys Met Tyr 20 25 Ala Met Lys Tyr Met Asn Lys Gln Gln Cys Ile Glu Arg Asp Glu Val 40 45 Arg Asn Val Phe Arg Glu Leu Glu Ile Leu Gln Glu Ile Glu His Val 55 60 Phe Leu Val Asn Leu Trp Tyr Ser Phe Gln Asp Glu Glu Asp Met Phe 70 75 Met Val Val Asp Leu Leu Gly Gly Asp Leu Arg Tyr His Leu Gln 90 Gln Asn Val Gln Phe Ser Glu Asp Thr Val Arg Leu Tyr Ile Cys Glu 105 Met Ala Leu Ala Leu Asp Tyr Leu Arg Ser Gln His Ile Ile His Arg 120. 125 Asp Val Lys Pro Asp Asn Ile Leu Leu Asp Glu Gln Gly His Ala His 135 140 Leu Thr Asp Phe Asn Ile Ala Thr Ile Ile Lys Asp Gly Glu Arg Ala 145 150 155

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Thr Ala Leu Ala Gly Thr Lys Pro Tyr Met Ala Pro Glu Ile Phe His
               165
                                  170
Ser Phe Val Asn Gly Gly Thr Gly Tyr Ser Phe Glu Val Asp Trp Trp
                               185
                                          190
Ser Val Gly Val Met Ala Tyr Glu Leu Leu Arg Gly Trp Arg Pro Tyr
Asp Ile His Ser Ser Asn Ala Val Glu Ser Leu Val Gln Leu Phe Ser
                  215
                                          220
Thr Val Ser Val Gln Tyr Val Pro Thr Trp Ser Lys Glu Met Val Ala
                   230
                                   . 235
Leu Leu Arg Lys Leu Leu Thr Val Asn Pro Glu His Arg Phe Ser Ser
               245
                                   250
Leu Gln Asp Met Gln Thr Ala Pro Ser Leu Ala His Val Leu Trp Asp
          260
                               265
Asp Leu Ser Glu Lys Lys Val Glu Pro Gly Phe Val Pro Asn Lys Gly
                           280
Arg Leu His Cys Asp Pro Thr Phe Glu Leu Glu Glu Met Ile Leu Glu
                       295
                                          300
Ser Arg Pro Leu His Lys Lys Lys Lys Arg Leu Ala Lys Asn Lys Ser
                                     : 315
                   310
Arg Asp Ser Ser Arg Asp Ser Ser Gln Ser Glu Asn Asp Tyr Leu Gln
               325
                                  330.
Asp Cys Leu Asp Ala Ile Gln Gln Asp Phe Val Ile Phe Asn Arg Glu
                              345.
Lys Leu Lys Arg Ser Gln Glu Leu Met Ser Glu Pro Pro Gly Pro
                          360
Glu Thr Ser Asp Met Thr Asp Ser Thr Ala Asp Ser Glu Ala Glu Pro
                      375
                             380
Thr Ala Leu Pro Met Cys Gly Ser Ile Cys Pro Ser Ser Gly Ser
                   390
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<210> 5

<211> 368

<212> PRT

<213> Macaca fascicularis

## <400> 5

Met Tyr Ala Met Lys Tyr Met Asn Lys Gln Gln Cys Ile Glu Arg Asp Glu Val Arg Asn Val Phe Arg Glu Leu Gly Ile Leu Gln Glu Ile Glu 20 25 His Val Phe Leu Val Asn Leu Trp Tyr Ser Phe Gln Asp Glu Glu Asp 40 Met Phe Met Val Val Asp Leu Leu Gly Gly Asp Leu Arg Tyr His 55 Leu Gln Gln Asn Val Gln Phe Ser Glu Asp Thr Val Arg Leu Tyr Ile 70 Cys Glu Met Ala Leu Ala Leu Asp Tyr Leu Cys Gly Gln His Ile Ile 85 90 His Arg Asp Val Lys Pro Asp Asn Ile Leu Leu Asp Glu Arg Gly His 105 Ala His Leu Thr Asp Phe Asn Ile Ala Thr Ile Ile Lys Asp Gly Glu 120 Arg Ala Thr Ala Leu Ala Gly Thr Lys Pro Tyr Met Ala Pro Glu Ile 135 140 Phe His Ser Phe Val Asn Gly Gly Thr. Gly Tyr Ser Phe Glu Val Asp

145					150					155					160
Trp	Trp	Ser	Leu	Gly 165	Val	Met	Ala	Tyr	Glu 170	Leu	Leu	Arg	Gly	Trp 175	Arg
Pro	Tyr	Asp	Ile 180	His	Ser	Ser	Asn	Ala 185	Val	Glu	Ser	Leu	Val 190	Gln	Leu
Phe	Ser	Thr 195	Val	Ser	Val	Gln	Tyr 200	Val	Pro	Thr	Trp	Ser 205	Arg	Glu	Met
Val	Ala 210					Leu 215					Pro 220	Glu	His	Arg	Phe
Ser 225	Ser		Gln	_	Val 230	Gln	Ala	Ala	Pro	Ala 235			Gly		
Trp	Gly	His	Leu	Ser 245	Glu	Lys	Arg		Glu 250	Pro	_	Phe	Val	Pro 255	Asn
Lys	Gly	Arg				Asp			Phe				Glu 270		Ile
Leu	Glu		Arg		Leu	His		Lys		Lys			Ala	Lys	Asn
Lys	Ser 290	Arg	Asp	Asn	Ser	Arg 295	_		Ser		Ser 300	Glu	Asn	Asp	Tyr
Leu 305	Gln	Asp	Cys	Leu	Asp 310	Ala	Ile			Asp 315	Phe		Ile	Phe	Asn 320
Arg	Glu	Lys	Leu	Lys 325	Arg	Ser	Gln	Asp		Pro		Glu	Pro	Leu 335	Pro
Ala	Pro	Glu				Ala		Glu 345		Val		Asp	Glu 350	Glu	Gln
Ser	Ala	Leu 355	Pro		Cys	Gly			Cys.			Ala 365	Gly	Ser	Gly